

## SEQUENCE LISTING

## (1) GENERAL INFORMATION:

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(i) APPLICANT: Genentech, Inc.  
Hsei, Vanessa  
Koumenis, Iphigenia  
Leong, Steven R.  
10 Presta, Leonard G.  
Shahrokh, Zahra  
Zapata, Gerardo A.

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(ii) TITLE OF INVENTION: Antibody Fragment-Polymer Conjugates and  
Humanized Anti-IL-8 Monoclonal Antibodies

(iii) NUMBER OF SEQUENCES: 72

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(iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Genentech, Inc.  
(B) STREET: 1 DNA Way  
(C) CITY: South San Francisco  
(D) STATE: California  
(E) COUNTRY: USA  
25 (F) ZIP: 94080

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(v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: WinPatin (Genentech)

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(vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE: 20-Feb-1998  
(C) CLASSIFICATION:

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(viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Love, Richard B.  
(B) REGISTRATION NUMBER: 34,659  
(C) REFERENCE/DOCKET NUMBER: P1085R3PCT

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(ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650/225-5530  
(B) TELEFAX: 650/952-9881

## (2) INFORMATION FOR SEQ ID NO:1:

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(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 22 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CAGTCCAACCT GTTCAGGACG CC 22

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(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GTGCTGCTCA TGCTGTAGGT GC 22

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 23 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GAAGTTGATG TCTTGTGAGT GGC 23

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 24 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GCATCCTAGA GTCACCGAGG AGCC 24

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CACTGGCTCA GGGAAATAAC CC 22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 22 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGAGAGCTGG GAAGGTGTGC AC 22

(2) INFORMATION FOR SEQ ID NO:7:

- 5 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACAAACGCGT ACGCTGACAT CGTCATGACC CAGTC 35

15 (2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: Nucleic Acid  
 20 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

25 ACAAACGCGT ACGCTGATAT TGTCATGACT CAGTC 35

(2) INFORMATION FOR SEQ ID NO:9:

- 30 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 35 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACAAACGCGT ACGCTGACAT CGTCATGACA CAGTC 35

40 (2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 37 base pairs  
 45 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

50 GCTCTTCGAA TGGTGGGAAG ATGGATACAG TTGGTGTC 37

55 (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 60 (D) TOPOLOGY: Linear

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CGATGGGCCC GGATAGACCG ATGGGGCTGT TGTTTTGGC 39

5 (2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: Nucleic Acid  
 10 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

15

CGATGGGCCC GGATAGACTG ATGGGGCTGT CGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:13:

20 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CGATGGGCCC GGATAGACGG ATGGGGCTGT TGTTTTGGC 39

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(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 35 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

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CGATGGGCCC GGATAGACAG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:15:

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(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 39 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 50 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

55 CGATGGGCCC GGATAGACTG ATGGGGCTGT TGTTTTGGC 39

(2) INFORMATION FOR SEQ ID NO:16:

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 369 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 GACATTGTCA TGACACAGTC TCAAAAATTC ATGTCCACAT CAGTAGGAGA 50  
 CAGGGTCAGC GTCACCTGCA AGGCCAGTCA GAATGTGGGT ACTAATGTAG 100  
 10 CCTGGTATCA ACAGAAACCA GGGCAATCTC CTAAAGCACT GATTTACTCG 150  
 TCATCCTACC GGTACAGTGG AGTCCCTGAT CGCTTCACAG GCAGTGGATC 200  
 TGGGACAGAT TTTACTCTCA CCATCAGCCA TGTGCAGTCT GAAGACTTGG 250  
 15 CAGACTATTT CTGTCAGCAA TATAACATCT ATCCTCTCAC GTTCGGTCCT 300  
 GGGACCAAGC TGGAGTTGAA ACGGGCTGAT GCTGCACCAC CAACTGTATC 350  
 20 CATCTTCCCA CCATTCGAA 369

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:  
 25 (A) LENGTH: 123 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

30 Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser Thr Ser Val  
     1                    5                    10                    15  
 35 Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val Gly  
                     20                    25                    30  
 Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
                     35                    40                    45  
 40 Ala Leu Ile Tyr Ser Ser Ser Tyr Arg Tyr Ser Gly Val Pro Asp  
                     50                    55                    60  
 Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile  
                     65                    70                    75  
 45 Ser His Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln  
                     80                    85                    90  
 50 Tyr Asn Ile Tyr Pro Leu Thr Phe Gly Pro Gly Thr Lys Leu Glu  
                     95                    100                    105  
 Leu Lys Arg Ala Asp Ala Ala Pro Pro Thr Val Ser Ile Phe Pro  
                     110                    115                    120  
 55 Pro Phe Glu  
                     123

(2) INFORMATION FOR SEQ ID NO:18:

60 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 417 base pairs  
 (B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

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TTCTATTGCT ACAAACGCGT ACGCTGAGGT GCAGCTGGTG GAGTCTGGGG 50  
GAGGCTTAGT GCCGCCTGGA GGGTCCCTGA AACTCTCCTG TGCAGCCTCT 100  
GGATTCATAT TCAGTAGTTA TGGCATGTCT TGGGTTCGCC AGACTCCAGG 150  
CAAGAGCCTG GAGTTGGTCG CAACCATTAA TAATAATGGT GATAGCACCT 200  
ATTATCCAGA CAGTGTGAAG GGCCGATTCA CCATCTCCCG AGACAATGCC 250  
AAGAACACCC TGTACCTGCA AATGAGCAGT CTGAAGTCTG AGGACACAGC 300  
CATGTTTTAC TGTGCAAGAG CCCTCATTAG TTCGGCTACT TGGTTTGGTT 350  
ACTGGGGCCA AGGGA CTCTG GTCAGTGTCT CTGCAGCCAA AACAACAGCC 400  
CCATCTGTCT ATCCGGG 417

25 (2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 130 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

35	Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Pro Pro Gly	1	5	10	15
	Gly Ser Leu Lys Leu Ser Cys Ala Ala Ser Gly Phe Ile Phe Ser	20	25	30	
40	Ser Tyr Gly Met Ser Trp Val Arg Gln Thr Pro Gly Lys Ser Leu	35	40	45	
	Glu Leu Val Ala Thr Ile Asn Asn Asn Gly Asp Ser Thr Tyr Tyr	50	55	60	
45	Pro Asp Ser Val Lys Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala	65	70	75	
	Lys Asn Thr Leu Tyr Leu Gln Met Ser Ser Leu Lys Ser Glu Asp	80	85	90	
	Thr Ala Met Phe Tyr Cys Ala Arg Ala Leu Ile Ser Ser Ala Thr	95	100	105	
55	Trp Phe Gly Tyr Trp Gly Gln Gly Thr Leu Val Thr Val Ser Ala	110	115	120	
	Ala Lys Thr Thr Ala Pro Ser Val Tyr Pro	125	130		

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(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACAAACGCGT ACGCTGATAT CGTCATGACA G 31

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 31 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GCAGCATCAG CTCTTCGAAG CTCCAGCTTG G 31

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 21 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCACTAGTAC GCAAGTTCAC G 21

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 33 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GATGGGCCCT TGGTGGAGGC TGCAGAGACA GTG 33

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 714 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTG TTTTTTCTAT 50

TGCTACAAAC GCGTACGCTG ATATCGTCAT GACACAGTCT CAAAAATTCA 100  
 TGTCCACATC AGTAGGAGAC AGGGTCAGCG TCACCTGCAA GGCCAGTCAG 150  
 5 AATGTGGGTA CTAATGTAGC CTGGTATCAA CAGAAACCAG GGCAATCTCC 200  
 TAAAGCACTG ATTTACTCGT CATCCTACCG GTACAGTGGA GTCCCTGATC 250  
 10 GCTTCACAGG CAGTGGATCT GGGACAGATT TCACTCTCAC CATCAGCCAT 300  
 GTGCAGTCTG AAGACTTGGC AGACTATTTT TGTGAGCAAT ATAACATCTA 350  
 TCCTCTCACG TTCGGTCCTG GGACCAAGCT GGAGCTTCGA AGAGCTGTGG 400  
 15 CTGCACCATC TGTCTTCATC TTCCCGCCAT CTGATGAGCA GTTGAAATCT 450  
 GGAAGTCTT CTGTTGTGTG CCTGCTGAAT AACTTCTATC CCAGAGAGGC 500  
 20 CAAAGTACAG TGGAAGGTGG ATAACGCCCT CCAATCGGGT AACTCCCAGG 550  
 AGAGTGTCAC AGAGCAGGAC AGCAAGGACA GCACCTACAG CCTCAGCAGC 600  
 ACCCTGACGC TGAGCAAAGC AGACTACGAG AAACACAAAG TCTACGCCTG 650  
 25 CGAAGTCACC CATCAGGGCC TGAGCTCGCC CGTCACAAAG AGCTTCAACA 700  
 GGGGAGAGTG TTAA 714

30 (2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 237 amino acids  
 (B) TYPE: Amino Acid  
 35 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

40	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Val	Met	Thr	Gln	Ser	20	25	30	
45	Gln	Lys	Phe	Met	Ser	Thr	Ser	Val	Gly	Asp	Arg	Val	Ser	Val	Thr	35	40	45	
	Cys	Lys	Ala	Ser	Gln	Asn	Val	Gly	Thr	Asn	Val	Ala	Trp	Tyr	Gln	50	55	60	
50	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Ala	Leu	Ile	Tyr	Ser	Ser	Ser	65	70	75	
55	Tyr	Arg	Tyr	Ser	Gly	Val	Pro	Asp	Arg	Phe	Thr	Gly	Ser	Gly	Ser	80	85	90	
	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	His	Val	Gln	Ser	Glu	Asp	95	100	105	
60	Leu	Ala	Asp	Tyr	Phe	Cys	Gln	Gln	Tyr	Asn	Ile	Tyr	Pro	Leu	Thr	110	115	120	



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	Phe	Gly	Pro	Gly	Thr	Lys	Leu	Glu	Leu	Arg	Arg	Ala	Val	Ala	Ala	
					125					130					135	
5	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	Glu	Gln	Leu	Lys	Ser	
					140					145					150	
	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	Asn	Phe	Tyr	Pro	Arg	
					155					160					165	
10	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	
					170					175					180	
	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	
					185					190					195	
15	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	
					200					205					210	
	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	
20					215					220					225	
	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys				
					230					235		237				

25 (2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 756 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

35	ATGAAAAAGA	ATATCGCATT	TCTTCTTGCA	TCTATGTTCTG	TTTTTCTAT	50
	TGCTACAAAC	GCGTACGCTG	AGGTGCAGCT	GGTGGAGTCT	GGGGGAGGCT	100
40	TAGTGCCGCC	TGGAGGGTCC	CTGAAACTCT	CCTGTGCAGC	CTCTGGATTCT	150
	ATATTTCAGTA	GTTATGGCAT	GTCTTGGGTT	CGCCAGACTC	CAGGCAAGAG	200
	CCTGGAGTTG	GTCGCAACCA	TTAATAATAA	TGGTGATAGC	ACCTATTATC	250
45	CAGACAGTGT	GAAGGGCCGA	TTCACCATCT	CCCGAGACAA	TGCCAAGAAC	300
	ACCCTGTACC	TGCAAATGAG	CAGTCTGAAG	TCTGAGGACA	CAGCCATGTT	350
50	TTACTGTGCA	AGAGCCCTCA	TTAGTTCGGC	TACTTGGTTT	GGTTACTGGG	400
	GCCAAGGGAC	TCTGGTCACT	GTCTCTGCAG	CCTCCACCAA	GGGCCCATCG	450
	GTCTTCCCCC	TGGCACCCCTC	CTCCAAGAGC	ACCTCTGGGG	GCACAGCGGC	500
55	CCTGGGCTGC	CTGGTCAAGG	ACTACTTCCC	CGAACCGGTG	ACGGTGTCTGT	550
	GGAACCTCAGG	CGCCCTGACC	AGCGGCGTGC	ACACCTTCCC	GGCTGTCCTA	600
60	CAGTCCTCAG	GACTCTACTC	CCTCAGCAGC	GTGGTGACCG	TGCCCTCCAG	650
	CAGCTTGGGC	ACCCAGACCT	ACATCTGCAA	CGTGAATCAC	AAGCCCAGCA	700

ACACCAAGGT GGACAAGAAA GTTGAGCCCA AATCTTGTGA CAAAACTCAC 750

ACATGA 756

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(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- 10 (A) LENGTH: 251 amino acids  
(B) TYPE: Amino Acid  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

15	Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe	1	5	10	15
	Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser	20	25	30	
20	Gly Gly Gly Leu Val Pro Pro Gly Gly Ser Leu Lys Leu Ser Cys	35	40	45	
	Ala Ala Ser Gly Phe Ile Phe Ser Ser Tyr Gly Met Ser Trp Val	50	55	60	
25	Arg Gln Thr Pro Gly Lys Ser Leu Glu Leu Val Ala Thr Ile Asn	65	70	75	
	Asn Asn Gly Asp Ser Thr Tyr Tyr Pro Asp Ser Val Lys Gly Arg	80	85	90	
	Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr Leu Gln	95	100	105	
35	Met Ser Ser Leu Lys Ser Glu Asp Thr Ala Met Phe Tyr Cys Ala	110	115	120	
	Arg Ala Leu Ile Ser Ser Ala Thr Trp Phe Gly Tyr Trp Gly Gln	125	130	135	
40	Gly Thr Leu Val Thr Val Ser Ala Ala Ser Thr Lys Gly Pro Ser	140	145	150	
	Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr	155	160	165	
45	Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu Pro Val	170	175	180	
	Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val His Thr	185	190	195	
50	Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu Ser Ser	200	205	210	
	Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr Tyr Ile	215	220	225	
55	Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp Lys Lys	230	235	240	

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Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr  
245 250 251

(2) INFORMATION FOR SEQ ID NO:28:

5

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

10

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

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CCAATGCATA CGCTGACATC GTGATGACCC AGACCCC 37

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

20

(D) TOPOLOGY: Linear

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CCAATGCATA CGCTGATATT GTGATGACTC AGACTCC 37

30

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 37 base pairs

(B) TYPE: Nucleic Acid

35

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

40

CCAATGCATA CGCTGACATC GTGATGACAC AGACACC 37

(2) INFORMATION FOR SEQ ID NO:31:

45

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

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(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

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AGATGTCAAT TGCTCACTGG ATGGTGGGAA GATGG 35

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 base pairs

60

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

5 CAAACGCGTA CGCTGAGATC CAGCTGCAGC AG 32

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:  
 10 (A) LENGTH: 32 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

CAAACGCGTA CGCTGAGATT CAGCTCCAGC AG 32

20 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 391 base pairs  
 (B) TYPE: Nucleic Acid  
 25 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

30 GATATCGTGA TGACACAGAC ACCACTCTCC CTGCCTGTCA GTCTTGGAGA 50  
 TCAGGCCTCC ATCTCTTGCA GATCTAGTCA GAGCCTTGTA CACGGTATTG 100  
 35 GAAACACCTA TTTACATTGG TACCTGCAGA AGCCAGGCCA GTCTCCAAAG 150  
 CTCCTGATCT ACAAAGTTTC CAACCGATTT TCTGGGGTCC CAGACAGGTT 200  
 CAGTGGCAGT GGATCAGGGA CAGATTTTAC ACTCAGGATC AGCAGAGTGG 250  
 40 AGGCTGAGGA TCTGGGACTT TATTTCTGCT CTCAAAGTAC ACATGTTCCG 300  
 CTCACGTTTC GTGCTGGGAC CAAGCTGGAG CTGAAACGGG CTGATGCTGC 350  
 45 ACCAACTGTA TCCATCTTCC CACCATCCAG TGAGCAATTG A 391

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:  
 50 (A) LENGTH: 131 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

55 Asp Ile Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val Ser Leu  
 1 5 10 15  
 60 Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Ser Gln Ser Leu Val  
 20 25 30  
 His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Leu Gln Lys Pro

	35	40	45
	Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe		
	50	55	60
5	Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp		
	65	70	75
	Phe Thr Leu Arg Ile Ser Arg Val Glu Ala Glu Asp Leu Gly Leu		
10	80	85	90
	Tyr Phe Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Ala		
	95	100	105
15	Gly Thr Lys Leu Glu Leu Lys Arg Ala Asp Ala Ala Pro Thr Val		
	110	115	120
	Ser Ile Phe Pro Pro Ser Ser Glu Gln Leu Lys		
	125	130 131	

## (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 405 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

GAGATTCAGC TGCAGCAGTC TGGACCTGAG CTGATGAAGC CTGGGGCTTC 50

AGTGAAGATA TCCTGCAAGG CTTCTGGTTA TTCATTTCAGT AGCCACTACA 100

35 TGCACCTGGGT GAAGCAGAGC CATGGAAAGA GCCTTGAGTG GATTGGCTAC 150

ATTGATCCTT CCAATGGTGA AACTACTTAC AACCAGAAAT TCAAGGGCAA 200

40 GGCCACATTG ACTGTAGACA CATCTTCCAG CACAGCCAAC GTGCATCTCA 250

GCAGCCTGAC ATCTGATGAC TCTGCACTCT ATTTCTGTGC AAGAGGGGAC 300

TATAGATACA ACGGCGACTG GTTTTTTCGAT GTCTGGGGCG CAGGGACCAC 350

45 GGTCACCGTC TCCTCCGCCA AAACCGACAG CCCCATCGGT CTATCCGGGC 400

CCATC 405

## (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 135 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Glu Ile Gln Leu Gln Gln Ser Gly Pro Glu Leu Met Lys Pro Gly			
1	5	10	15
Ala Ser Val Lys Ile Ser Cys Lys Ala Ser Gly Tyr Ser Phe Ser			

	20	25	30
	Ser His Tyr Met His Trp Val Lys Gln	Ser His Gly Lys Ser Leu	
	35	40	45
5	Glu Trp Ile Gly Tyr Ile Asp Pro Ser Asn	Gly Glu Thr Thr Tyr	
	50	55	60
10	Asn Gln Lys Phe Lys Gly Lys Ala Thr Leu	Thr Val Asp Thr Ser	
	65	70	75
	Ser Ser Thr Ala Asn Val His Leu Ser Ser	Leu Thr Ser Asp Asp	
	80	85	90
15	Ser Ala Val Tyr Phe Cys Ala Arg Gly Asp	Tyr Arg Tyr Asn Gly	
	95	100	105
	Asp Trp Phe Phe Asp Val Trp Gly Ala Gly	Thr Thr Val Thr Val	
	110	115	120
20	Ser Ser Ala Lys Thr Asp Ser Pro Ile Gly	Leu Ser Gly Pro Ile	
	125	130	135

## (2) INFORMATION FOR SEQ ID NO:38:

25

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

35

CTTGGTGGAG GCGGAGGAGA CG 22

## (2) INFORMATION FOR SEQ ID NO:39:

40

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 38 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

45

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GAAACGGGCT GTTGCTGCAC CAACTGTATT CATCTTCC 38

50

## (2) INFORMATION FOR SEQ ID NO:40:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 31 base pairs

(B) TYPE: Nucleic Acid

55

(C) STRANDEDNESS: Single

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

60

GTCACCGTCT CCTCCGCCTC CACCAAGGGC C 31

## (2) INFORMATION FOR SEQ ID NO:41:

## (i) SEQUENCE CHARACTERISTICS:

- 5 (A) LENGTH: 729 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Double  
 (D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ATGAAGAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50  
 TGCTACAAAT GCATACGCTG ATATCGTGAT GACACAGACA CCACTCTCCC 100  
 15 TGCCTGTCAG TCTTGGAGAT CAGGCCTCCA TCTCTTGCA GATCTAGTCAG 150  
 AGCCTTGTAC ACGGTATTGG AAACACCTAT TTACATTGGT ACCTGCAGAA 200  
 20 GCCAGGCCAG TCTCCAAAGC TCCTGATCTA CAAAGTTTCC AACCGATTTT 250  
 CTGGGGTCCC AGACAGGTTC AGTGGCAGTG GATCAGGGAC AGATTTTACA 300  
 CTCAGGATCA GCAGAGTGGA GGCTGAGGAT CTGGGACTTT ATTTCTGCTC 350  
 25 TCAAAGTACA CATGTTCCGC TCACGTTCCG TGCTGGGACC AAGCTGGAGC 400  
 TGAAACGGGC TGTGCTGCA CCAACTGTAT TCATCTTCCC ACCATCCAGT 450  
 30 GAGCAATTGA AATCTGGAAC TGCCTCTGTT GTGTGCCTGC TGAATAACTT 500  
 CTATCCCAGA GAGGCCAAAG TACAGTGGA GGTGGATAAC GCCCTCCAAT 550  
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600  
 35 TACAGCCTCA GCAGCACCT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
 CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGCCTGAGC TCGCCCGTCA 700  
 40 CAAAGAGCTT CAACAGGGGA GAGTGTTAA 729

## (2) INFORMATION FOR SEQ ID NO:42:

## (i) SEQUENCE CHARACTERISTICS:

- 45 (A) LENGTH: 242 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Val Met Thr Gln Thr  
 55 20 25 30  
 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser  
 35 40 45  
 60 Cys Arg Ser Ser Gln Ser Leu Val His Gly Ile Gly Asn Thr Tyr  
 50 55 60

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	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	Gly	Gln	Ser	Pro	Lys	Leu	Leu	
					65					70					75	
5	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	
					80					85					90	
	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	
					95					100					105	
10	Val	Glu	Ala	Glu	Asp	Leu	Gly	Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	
					110					115					120	
	His	Val	Pro	Leu	Thr	Phe	Gly	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	
15					125					130					135	
	Arg	Ala	Val	Ala	Ala	Pro	Thr	Val	Phe	Ile	Phe	Pro	Pro	Ser	Ser	
					140					145					150	
20	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	
					155					160					165	
	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	
					170					175					180	
25	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
					185					190					195	
	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
30					200					205					210	
	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	
					215					220					225	
35	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	
					230					235					240	
	Glu	Cys														
		242														

40 (2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 762 base pairs  
(B) TYPE: Nucleic Acid  
45 (C) STRANDEDNESS: Double  
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

50 ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT 50  
TGCTACAAAC GCGTACGCTG AGATTCAGCT GCAGCAGTCT GGACCTGAGC 100  
55 TGATGAAGCC TGGGGCTTCA GTGAAGATAT CCTGCAAGGC TTCTGGTTAT 150  
TCATTACAGTA GCCACTACAT GCACTGGGTG AAGCAGAGCC ATGGAAAGAG 200  
CCTTGAGTGG ATTGGCTACA TTGATCCTTC CAATGGTGAA ACTACTTACA 250  
60 ACCAGAAATT CAAGGGCAAG GCCACATTGA CTGTAGACAC ATCTTCCAGC 300



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ACAGCCAACG TGCATCTCAG CAGCCTGACA TCTGATGACT CTGCAGTCTA 350  
 TTTCTGTGCA AGAGGGGACT ATAGATACAA CGGCGACTGG TTTTTCGATG 400  
 5 TCTGGGGCGC AGGGACCACG GTCACCGTCT CCTCCGCCTC CACCAAGGGC 450  
 CCATCGGTCT TCCCCCTGGC ACCCTCCTCC AAGAGCACCT CTGGGGGCAC 500  
 AGCGGGCCCTG GGCTGCCTGG TCAAGGACTA CTTCCCCGAA CCGGTGACGG 550  
 10 TGTCGTGGAA CTCAGGCGCC CTGACCAGCG GCGTGCACAC CTTCCCGGCT 600  
 GTCCTACAGT CCTCAGGACT CTACTCCCTC AGCAGCGTGG TGACCGTGCC 650  
 15 CTCCAGCAGC TTGGGCACCC AGACCTACAT CTGCAACGTG AATCACAAGC 700  
 CCAGCAACAC CAAGGTGGAC AAGAAAGTTG AGCCCAAATC TTGTGACAAA 750  
 ACTCACACAT GA 762

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 253 amino acids  
 25 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

30 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
     1                    5                    10                    15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Ile Gln Leu Gln Gln Ser  
                     20                    25                    30  
 35 Gly Pro Glu Leu Met Lys Pro Gly Ala Ser Val Lys Ile Ser Cys  
                     35                    40                    45  
 Lys Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val  
 40                    50                    55                    60  
 Lys Gln Ser His Gly Lys Ser Leu Glu Trp Ile Gly Tyr Ile Asp  
                     65                    70                    75  
 45 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Lys  
                     80                    85                    90  
 Ala Thr Leu Thr Val Asp Thr Ser Ser Ser Thr Ala Asn Val His  
                     95                    100                    105  
 50 Leu Ser Ser Leu Thr Ser Asp Asp Ser Ala Val Tyr Phe Cys Ala  
                     110                    115                    120  
 Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp  
 55                    125                    130                    135  
 Gly Ala Gly Thr Thr Val Thr Val Ser Ser Ala Ser Thr Lys Gly  
                     140                    145                    150  
 60 Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly  
                     155                    160                    165

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	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	170	175	180
5	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	Gly	Ala	Leu	Thr	Ser	Gly	Val	185	190	195
	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	200	205	210
10	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	Leu	Gly	Thr	Gln	Thr	215	220	225
	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	Thr	Lys	Val	Asp	230	235	240
15	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	Asp	Lys	Thr	His	Thr			245	250	253

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

30	Asp	Ile	Val	Met	Thr	Gln	Thr	Pro	Leu	Ser	Leu	Pro	Val	Ser	Leu	1	5	10	15
	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	20	25	30	
35	His	Gly	Ile	Gly	Asn	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro	35	40	45	
	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Tyr	Lys	Val	Ser	Asn	Arg	50	55	60	
40	Phe	Ser	Gly	Val	Pro	Asp	Arg	Phe	Ser	Asp	Ser	Gly	Ser	Gly	Thr	65	70	75	
	Asp	Phe	Thr	Leu	Arg	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	80	85	90	
45	Leu	Tyr	Phe	Cys	Ser	Gln	Ser	Thr	His	Val	Pro	Leu	Thr	Phe	Gly	95	100	105	
50	Ala	Gly	Thr	Lys	Leu	Glu	Leu	Lys	Arg							110	114		

(2) INFORMATION FOR SEQ ID NO:46:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 114 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

60	Asp	Ile	Gln	Met	Thr	Gln	Ser	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	1	5	10	15
----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val  
                             20                            25                            30  
 5 His Gly Ile Gly Asn Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro  
                             35                            40                            45  
 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Tyr Lys Val Ser Asn Arg  
                             50                            55                            60  
 10 Phe Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr  
                             65                            70                            75  
 Asp Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala  
 15                            80                            85                            90  
 Thr Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly  
                             95                            100                            105  
 20 Gln Gly Thr Lys Val Glu Ile Lys Arg  
                             110                            114

## (2) INFORMATION FOR SEQ ID NO:47:

25 (i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 109 amino acids  
       (B) TYPE: Amino Acid  
       (D) TOPOLOGY: Linear

## 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val  
   1                            5                            10                            15  
 35 Gly Asp Arg Val Thr Ile Thr Cys Arg Ala Ser Lys Thr Ile Ser  
                             20                            25                            30  
 Lys Tyr Leu Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
                             35                            40                            45  
 40 Leu Leu Ile Tyr Tyr Ser Gly Ser Thr Leu Glu Ser Gly Val Pro  
                             50                            55                            60  
 Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr  
 45                            65                            70                            75  
 Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr Tyr Tyr Cys Gln  
                             80                            85                            90  
 50 Gln His Asn Glu Tyr Pro Leu Thr Phe Gly Gln Gly Thr Lys Val  
                             95                            100                            105  
 Glu Ile Lys Arg  
                             109

55

## (2) INFORMATION FOR SEQ ID NO:48:

(i) SEQUENCE CHARACTERISTICS:  
       (A) LENGTH: 117 amino acids  
       (B) TYPE: Amino Acid  
       (D) TOPOLOGY: Linear

60

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

5	Glu	Ile	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Met	Lys	Pro	Gly	1	5	10	15
	Ala	Ser	Val	Lys	Ile	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30	
10	Ser	His	Tyr	Met	His	Trp	Val	Lys	Gln	Ser	His	Gly	Lys	Ser	Leu	35	40	45	
	Glu	Trp	Ile	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60	
15	Asn	Gln	Lys	Phe	Lys	Gly	Lys	Ala	Thr	Leu	Thr	Val	Asp	Thr	Ser	65	70	75	
	Ser	Ser	Thr	Ala	Asn	Val	His	Leu	Ser	Ser	Leu	Thr	Ser	Asp	Asp	80	85	90	
20	Ser	Ala	Val	Tyr	Phe	Cys	Ala	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	95	100	105	
25	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Ala	Gly	Thr				110	115	117	

(2) INFORMATION FOR SEQ ID NO:49:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 117 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

35	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	1	5	10	15
40	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	20	25	30	
	Ser	His	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	35	40	45	
45	Glu	Trp	Val	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	50	55	60	
	Asn	Gln	Lys	Phe	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	65	70	75	
50	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	80	85	90	
55	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	95	100	105	
	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr				110	115	117	

60 (2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

	Glu	Val	Gln	Leu	Val	Glu	Ser	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	
	1				5					10					15	
10	Gly	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Ser	Phe	Thr	
					20					25					30	
	Gly	His	Trp	Met	Asn	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
					35					40					45	
15	Glu	Trp	Val	Gly	Met	Ile	His	Pro	Ser	Asp	Ser	Glu	Thr	Arg	Tyr	
					50					55					60	
	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	Ile	Ser	Arg	Asp	Asn	Ser	
20					65					70					75	
	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
					80					85					90	
25	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Ala	Arg	Gly	Ile	Tyr	Phe	Tyr	Gly	
					95					100					105	
	Thr	Thr	Tyr	Phe	Asp	Tyr	Trp	Gly	Gln	Gly	Thr					
					110					115	116					

(2) INFORMATION FOR SEQ ID NO:51:

(i) SEQUENCE CHARACTERISTICS:

35 (A) LENGTH: 242 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

40	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
	1				5					10					15	
	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	
					20					25					30	
45	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	
					35					40					45	
	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Asn	Thr	Tyr	
50					50					55					60	
	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	
					65					70					75	
55	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	
					80					85					90	
	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	
					95					100					105	
60	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	
					110					115					120	

	His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	
					125					130					135	
5	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	
					140					145					150	
	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	
					155					160					165	
10	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	
					170					175					180	
	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
15					185					190					195	
	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
					200					205					210	
20	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	
					215					220					225	
	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	
					230					235					240	
25	Glu	Cys														
					242											

## (2) INFORMATION FOR SEQ ID NO:52:

30

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 253 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

35

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

	Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	
	1				5					10					15	
40	Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Glu	Val	Gln	Leu	Val	Gln	Ser	
					20					25					30	
	Gly	Gly	Gly	Leu	Val	Gln	Pro	Gly	Gly	Ser	Leu	Arg	Leu	Ser	Cys	
45					35					40					45	
	Ala	Ala	Ser	Gly	Tyr	Ser	Phe	Ser	Ser	His	Tyr	Met	His	Trp	Val	
					50					55					60	
50	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Gly	Tyr	Ile	Asp	
					65					70					75	
	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	Asn	Gln	Lys	Phe	Lys	Gly	Arg	
					80					85					90	
55	Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	
					95					100					105	
	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	
60					110					115					120	
	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	Asp	Trp	Phe	Phe	Asp	Val	Trp	

		125		130		135
	Gly Gln Gly Thr	Leu Val Thr Val Ser	Ser Ala Ser Thr Lys Gly			
		140	145		150	
5	Pro Ser Val Phe	Pro Leu Ala Pro Ser	Ser Lys Ser Thr Ser Gly			
		155	160		165	
	Gly Thr Ala Ala	Leu Gly Cys Leu Val	Lys Asp Tyr Phe Pro Glu			
10		170	175		180	
	Pro Val Thr Val	Ser Trp Asn Ser Gly	Ala Leu Thr Ser Gly Val			
		185	190		195	
15	His Thr Phe Pro	Ala Val Leu Gln Ser	Ser Gly Leu Tyr Ser Leu			
		200	205		210	
	Ser Ser Val Val	Thr Val Pro Ser Ser	Ser Leu Gly Thr Gln Thr			
20		215	220		225	
	Tyr Ile Cys Asn	Val Asn His Lys Pro	Ser Asn Thr Lys Val Asp			
		230	235		240	
25	Lys Lys Val Glu	Pro Lys Ser Cys Asp	Lys Thr His Thr			
		245	250		253	

## (2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

30 (A) LENGTH: 159 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

35	Ser Gly Gly Gly Ser Gly Ser Gly Asp Phe Asp Tyr Glu Lys Met	
	1 5 10 15	
40	Ala Asn Ala Asn Lys Gly Ala Met Thr Glu Asn Ala Asp Glu Asn	
	20 25 30	
	Ala Leu Gln Ser Asp Ala Lys Gly Lys Leu Asp Ser Val Ala Thr	
	35 40 45	
45	Asp Tyr Gly Ala Ala Ile Asp Gly Phe Ile Gly Asp Val Ser Gly	
	50 55 60	
	Leu Ala Asn Gly Asn Gly Ala Thr Gly Asp Phe Ala Gly Ser Ser	
50	65 70 75	
	Asn Ser Gln Met Ala Gln Val Gly Asp Gly Asp Asn Ser Pro Leu	
	80 85 90	
55	Met Asn Asn Phe Arg Gln Tyr Leu Pro Ser Leu Pro Gln Ser Val	
	95 100 105	
	Glu Cys Arg Pro Phe Val Phe Ser Ala Gly Lys Pro Tyr Glu Phe	
	110 115 120	
60	Ser Ile Asp Cys Asp Lys Ile Asn Leu Phe Arg Gly Val Phe Ala	
	125 130 135	

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Phe Leu Leu Tyr Val Ala Thr Phe Met Tyr Val Phe Ser Thr Phe  
140 145 150

5 Ala Asn Ile Leu Arg Asn Lys Glu Ser  
155 159

(2) INFORMATION FOR SEQ ID NO:54:

10 (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 780 base pairs  
(B) TYPE: Nucleic Acid  
(C) STRANDEDNESS: Single  
(D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50  
20 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100  
TGTC CGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150  
AGCTTAGTAC ATGGTATAGG TAACACGTAT TTACACTGGT ATCAACAGAA 200  
25 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250  
CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300  
30 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350  
ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400  
TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450  
35 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500  
CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
40 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600  
TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
45 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750  
CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

50 (2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 253 amino acids  
(B) TYPE: Amino Acid  
55 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

60 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
1 5 10 15

Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Glu Ser



	20	25	30
	Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys		
	35	40	45
5	Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val		
	50	55	60
10	Lys Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp		
	65	70	75
	Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg		
	80	85	90
15	Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln		
	95	100	105
	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
	110	115	120
20	Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp		
	125	130	135
	Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
25	140	145	150
	Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly		
	155	160	165
30	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu		
	170	175	180
	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val		
	185	190	195
35	His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu		
	200	205	210
	Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
40	215	220	225
	Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
	230	235	240
45	Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr		
	245	250	253

## (2) INFORMATION FOR SEQ ID NO:56:

- 50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 242 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear
- 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe		
1	5	10
Ser Ile Ala Thr Asn Ala Tyr Ala Asp Ile Gln Met Thr Gln Ser		
20	25	30

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	Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	
					35					40					45	
5	Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Ala	Thr	Tyr	
					50					55					60	
	Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	
					65					70					75	
10	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	
					80					85					90	
	Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	
					95					100					105	
15	Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	
					110					115					120	
	His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	
20					125					130					135	
	Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	
					140					145					150	
25	Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	
					155					160					165	
	Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	
					170					175					180	
30	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	
					185					190					195	
	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	
35					200					205					210	
	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	
					215					220					225	
40	His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	
					230					235					240	
	Glu	Cys														
		242														

45

(2) INFORMATION FOR SEQ ID NO:57:

	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 45 amino acids
50	(B) TYPE: Amino Acid
	(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

55	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	Gly	Gly	Arg	Met	Lys	
	1				5						10				15	
	Gln	Leu	Glu	Asp	Lys	Val	Glu	Glu	Leu	Leu	Ser	Lys	Asn	Tyr	His	
					20					25					30	
60	Leu	Glu	Asn	Glu	Val	Ala	Arg	Leu	Lys	Lys	Leu	Val	Gly	Glu	Arg	
					35					40					45	

(2) INFORMATION FOR SEQ ID NO:58:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTCCTAT 50
TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100
TGTCCGCCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150
AGCTTAGTAC ATGGTATAGG TGCTACGTAT TTACACTGGT ATCAACAGAA 200
ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250
CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300
CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350
ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400
TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450
GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500
CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550
CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600
TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650
CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700
CAAAGAGCTT CAACAGGGGA GAGTGTAAAG CTGATCCTCT ACGCCGGACG 750
CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780
  
```

(2) INFORMATION FOR SEQ ID NO:59:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 927 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```

AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50
TCTTCTTGCA TCTATGTTTCG TTTTTCCTAT TGCTACAAAC GCGTACGCTG 100
AGGTTTCAGCT AGTGCAGTCT GGCGGTGGCC TGGTGCAGCC AGGGGGCTCA 150
CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACATAT 200
  
```

GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250  
 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300  
 5 TTCACCTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350  
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400  
 10 ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450  
 GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500  
 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550  
 15 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600  
 CTGACCAGCG GCGTGACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650  
 20 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700  
 AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750  
 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCGTG 800  
 25 CCCAGCACCA GAACTGCTGG GCGGCCGCAT GAAACAGCTA GAGGACAAGG 850  
 TCGAAGAGCT ACTCTCCAAG AACTACCACC TAGAGAATGA AGTGGCAAGA 900  
 30 CTCAAAAAGC TTGTCGGGGA GCGCTAA 927

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:  
 35 (A) LENGTH: 298 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

40 Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser  
 45 20 25 30  
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys  
 35 40 45  
 50 Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val  
 50 55 60  
 Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp  
 65 70 75  
 55 Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg  
 80 85 90  
 Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln  
 60 95 100 105  
 Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala

		110		115		120
	Arg Gly Asp Tyr	Arg Tyr Asn Gly Asp	Trp Phe Phe Asp Val	Trp		
		125		130		135
5	Gly Gln Gly Thr	Leu Val Thr Val Ser	Ser Ala Ser Thr Lys	Gly		
		140		145		150
	Pro Ser Val Phe	Pro Leu Ala Pro Ser	Ser Lys Ser Thr Ser	Gly		
10		155		160		165
	Gly Thr Ala Ala	Leu Gly Cys Leu Val	Lys Asp Tyr Phe Pro	Glu		
		170		175		180
15	Pro Val Thr Val	Ser Trp Asn Ser Gly	Ala Leu Thr Ser Gly	Val		
		185		190		195
	His Thr Phe Pro	Ala Val Leu Gln Ser	Ser Gly Leu Tyr Ser	Leu		
20		200		205		210
	Ser Ser Val Val	Thr Val Pro Ser Ser	Ser Leu Gly Thr Gln	Thr		
		215		220		225
	Tyr Ile Cys Asn	Val Asn His Lys Pro	Ser Asn Thr Lys Val	Asp		
25		230		235		240
	Lys Lys Val Glu	Pro Lys Ser Cys Asp	Lys Thr His Thr Cys	Pro		
		245		250		255
30	Pro Cys Pro Ala	Pro Glu Leu Leu Gly	Gly Arg Met Lys Gln	Leu		
		260		265		270
	Glu Asp Lys Val	Glu Glu Leu Leu Ser	Lys Asn Tyr His Leu	Glu		
		275		280		285
35	Asn Glu Val Ala	Arg Leu Lys Lys Leu	Val Gly Glu Arg			
		290		295		298

## (2) INFORMATION FOR SEQ ID NO:61:

- 40 (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 6563 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - 45 (D) TOPOLOGY: Linear
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

50 GAATTCAACT TCTCCATACT TTGGATAAGG AAATACAGAC ATGAAAAATC 50

TCATTGCTGA GTTGTTATTT AAGCTTGCCC AAAAAGAAGA AGAGTCGAAT 100

GAAGTGTGTG CGCAGGTAGA AGCTTTGGAG ATTATCGTCA CTGCAATGCT 150

55 TCGCAATATG GCGCAAAATG ACCAACAGCG GTTGATTGAT CAGGTAGAGG 200

GGGCGCTGTA CGAGGTAAAG CCCGATGCCA GCATTCCTGA CGACGATACG 250

60 GAGCTGCTGC GCGATTACGT AAAGAAGTTA TTGAAGCATC CTCGTCAGTA 300

AAAAGTTAAT CTTTTCAACA GCTGTCATAA AGTTGTCACG GCCGAGACTT 350

ATAGTCGCTT TGTTTTTATT TTTTAATGTA TTTGTAACTA GAATTCGAGC 400  
 5 TCGGTACCCG GGGATCCTCT CGAGGTTGAG GTGATTTTAT GAAAAAGAAT 450  
 ATCGCATTTT TTCTTGCATC TATGTTTCGTT TTTTCTATTG CTACAAACGC 500  
 ATACGCTGAT ATCCAGATGA CCCAGTCCCC GAGCTCCCTG TCCGCCTCTG 550  
 10 TGGGCGATAG GGTCAACCATC ACCTGCAGGT CAAGTCAAAG CTTAGTACAT 600  
 GGTATAGGTG CTACGTATTT ACACTGGTAT CAACAGAAAC CAGGAAAAGC 650  
 15 TCCGAAACTA CTGATTTACA AAGTATCCAA TCGATTCTCT GGAGTCCCTT 700  
 CTCGCTTCTC TGGATCCGGT TCTGGGACGG ATTTCACTCT GACCATCAGC 750  
 AGTCTGCAGC CAGAAGACTT CGCAACTTAT TACTGTTTAC AGAGTACTCA 800  
 20 TGTCCCGCTC ACGTTTGGAC AGGGTACCAA GGTGGAGATC AAACGAACTG 850  
 TGGCTGCACC ATCTGTCTTC ATCTTCCCGC CATCTGATGA GCAGTTGAAA 900  
 TCTGGAAGTG CTTCTGTTGT GTGCCTGCTG AATAACTTCT ATCCCAGAGA 950  
 25 GGCCAAAGTA CAGTGAAGG TGGATAACGC CCTCCAATCG GGTAAGTCCC 1000  
 AGGAGAGTGT CACAGAGCAG GACAGCAAGG ACAGCACCTA CAGCCTCAGC 1050  
 30 AGCACCTTGA CGCTGAGCAA AGCAGACTAC GAGAAACACA AAGTCTACGC 1100  
 CTGCGAAGTC ACCCATCAGG GCCTGAGCTC GCCCGTCACA AAGAGCTTCA 1150  
 ACAGGGGAGA GTGTTAAGCT GATCCTCTAC GCCGGACGCA TCGTGGCCCT 1200  
 35 AGTACGCAAC TAGTCGTAAG AAGGGTATCT AGAGGTTGAG GTGATTTTAT 1250  
 GAAAAAGAAT ATCGCATTTT TTCTTGCATC TATGTTTCGTT TTTTCTATTG 1300  
 40 CTACAAACGC GTACGCTGAG GTTCAGCTAG TGCAGTCTGG CGGTGGCCTG 1350  
 GTGCAGCCAG GGGGCTCACT CCGTTTGTCC TGTGCAGCTT CTGGCTACTC 1400  
 CTTCTCGAGT CACTATATGC ACTGGGTCCG TCAGGCCCCG GGTAAGGGCC 1450  
 45 TGAATGGGT TGGATATATT GATCCTTCCA ATGGTGAAAC TACGTATAAT 1500  
 CAAAAGTTCA AGGGCCGTTT CACTTTATCT CGCGACAACT CCAAAAACAC 1550  
 50 AGCATACCTG CAGATGAACA GCCTGCGTGC TGAGGACACT GCCGTCTATT 1600  
 ACTGTGCAAG AGGGGATTAT CGCTACAATG GTGACTGGTT CTTGACGTC 1650  
 TGGGGTCAAG GAACCCTGGT CACCGTCTCC TCGGCCTCCA CCAAGGGCCC 1700  
 55 ATCGGTCTTC CCCCTGGCAC CCTCCTCCAA GAGCACCTCT GGGGGCACAG 1750  
 CGGCCCTGGG CTGCCTGGTC AAGGACTACT TCCCCGAACC GGTGACGGTG 1800  
 60 TCGTGGAAGT CAGGCGCCCT GACCAGCGGC GTGCACACCT TCCCGGCTGT 1850  
 CCTACAGTCC TCAGGACTCT ACTCCCTCAG CAGCGTGGTG ACCGTGCCCT 1900

CCAGCAGCTT GGGCACCCAG ACCTACATCT GCAACGTGAA TCACAAGCCC 1950  
 5 AGCAACACCA AGGTGACAA GAAAGTTGAG CCCAAATCTT GTGACAAAAC 2000  
 TCACACATGC CCGCCGTGCC CAGCACCAGA ACTGCTGGGC GGCCGCATGA 2050  
 AACAGCTAGA GGACAAGGTC GAAGAGCTAC TCTCCAAGAA CTACCACCTA 2100  
 10 GAGAATGAAG TGGCAAGACT CAAAAAGCTT GTCGGGGAGC GCTAAGCATG 2150  
 CGACGGCCCT AGAGTCCCTA ACGCTCGGTT GCCGCCGGGC GTTTTTTATT 2200  
 GTTAACTCAT GTTTGACAGC TTATCATCGA TAAGCTTTAA TGCGGTAGTT 2250  
 15 TATCACAGTT AAATTGCTAA CGCAGTCAGG CACCGTGTAT GAAATCTAAC 2300  
 AATGCGCTCA TCGTCATCCT CGGCACCGTC ACCCTGGATG CTGTAGGCAT 2350  
 20 AGGCTTGTT ATGCCGGTAC TGCCGGGCCT CTTGCGGGAT ATCGTCCATT 2400  
 CCGACAGCAT CGCCAGTCAC TATGGCGTGC TGCTAGCGCT ATATGCGTTG 2450  
 ATGCAATTTT TATGCGCACC CGTTCTCGGA GCACTGTCCG ACCGCTTTGG 2500  
 25 CCGCCGCCCA GTCCTGCTCG CTTGCTACT TGGAGCCACT ATCGACTACG 2550  
 CGATCATGGC GACCACACCC GTCCTGTGGA TCCTCTACGC CGGACGCATC 2600  
 30 GTGGCCGGCA TCACCGGCGC CACAGGTGCG GTTGCTGGCG CCTATATCGC 2650  
 CGACATCACC GATGGGGAAG ATCGGGCTCG CCACTTCGGG CTCATGAGCG 2700  
 CTTGTTTCGG CGTGGGTATG GTGGCAGGCC CCGTGGCCGG GGGACTGTTG 2750  
 35 GGCGCCATCT CTTGACGC ACCATTCTT GCGGCGGCGG TGCTCAACGG 2800  
 CCTCAACCTA CTACTGGGCT GCTTCCTAAT GCAGGAGTCG CATAAGGGAG 2850  
 40 AGCGTCGTCC GATGCCCTTG AGAGCCTTCA ACCCAGTCAG CTCCTTCCGG 2900  
 TGGGCGCGGG GCATGACTAT CGTCGCCGCA CTTATGACTG TCTTCTTTAT 2950  
 CATGCAACTC GTAGGACAGG TGCCGGCAGC GCTCTGGGTC ATTTTCGGCG 3000  
 45 AGGACCGCTT TCGCTGGAGC GCGACGATGA TCGGCCTGTC GCTTGCGGTA 3050  
 TTCGGAATCT TGCACGCCCT CGCTCAAGCC TTCGTCACTG GTCCCGCCAC 3100  
 50 CAAACGTTTC GGCGAGAAGC AGGCCATTAT CGCCGGCATG GCGGCCGACG 3150  
 CGCTGGGCTA CGTCTTGCTG GCGTTCGCGA CGCGAGGCTG GATGGCCTTC 3200  
 CCCATTATGA TTCTTCTCGC TTCCGGCGGC ATCGGGATGC CCGCGTTGCA 3250  
 55 GGCCATGCTG TCCAGGACAGG TAGATGACGA CCATCAGGGA CAGCTTCAAG 3300  
 GATCGCTCGC GGCTCTTACC AGCCTAACTT CGATCACTGG ACCGCTGATC 3350  
 60 GTCACGGCGA TTTATGCCGC CTCGGCGAGC ACATGGAACG GGTTGGCATG 3400  
 GATTGTAGGC GCCGCCCTAT ACCTTGTCTG CCTCCCCGCG TTGCGTCGCG 3450

GTGCATGGAG CCGGGCCACC TCGACCTGAA TGGAAGCCGG CGGCACCTCG 3500  
 5 CTAACGGATT CACCACTCCA AGAATTGGAG CCAATCAATT CTTGCGGAGA 3550  
 ACTGTGAATG CGCAAACCAA CCCTTGGCAG AACATATCCA TCGCGTCCGC 3600  
 CATCTCCAGC AGCCGCACGC GGCATCTC GGGCAGCGTT GGGTCCTGGC 3650  
 10 CACGGGTGCG CATGATCGTG CTCCTGTCGT TGAGGACCCG GCTAGGCTGG 3700  
 CGGGGTGCG TTACTGGTTA GCAGAATGAA TCACCGATAC GCGAGCGAAC 3750  
 GTGAAGCGAC TGCTGCTGCA AAACGTCTGC GACCTGAGCA ACAACATGAA 3800  
 15 TGGTCTTCGG TTTCCGTGTT TCGTAAAGTC TGGAAACGCG GAAGTCAGCG 3850  
 CCCTGCACCA TTATGTTCCG GATCTGCATC GCAGGATGCT GCTGGCTACC 3900  
 20 CTGTGGAACA CCTACATCTG TATTAACGAA GCGCTGGCAT TGACCCTGAG 3950  
 TGATTTTCT CTGGTCCCGC CGCATCCATA CCGCCAGTTG TTTACCCTCA 4000  
 CAACGTTCCA GTAACCGGGC ATGTTTCATCA TCAGTAACCC GTATCGTGAG 4050  
 25 CATCCTCTCT CGTTTCATCG GTATCATTAC CCCCATGAAC AGAAATTCCC 4100  
 CCTTACACGG AGGCATCAAG TGACCAAACA GGAAAAAACC GCCCTTAACA 4150  
 30 TGGCCCGCTT TATCAGAAGC CAGACATTAA CGCTTCTGGA GAAACTCAAC 4200  
 GAGCTGGACG CGGATGAACA GGCAGACATC TGTGAATCGC TTCACGACCA 4250  
 CGCTGATGAG CTTTACCGCA GCTGCCTCGC GCGTTTCGGT GATGACGGTG 4300  
 35 AAAACCTCTG ACACATGCAG CTCCCGGAGA CGGTCACAGC TTGTCTGTAA 4350  
 GCGGATGCCG GGAGCAGACA AGCCCGTCAG GCGCGTCAG CGGGTGTTGG 4400  
 40 CGGGTGTCGG GGCAGACCA TGACCCAGTC ACGTAGCGAT AGCGGAGTGT 4450  
 ATACTGGCTT AACTATGCGG CATCAGAGCA GATTGTACTG AGAGTGCACC 4500  
 ATATGCGGTG TGAAATACCG CACAGATGCG TAAGGAGAAA ATACCGCATC 4550  
 45 AGGCGCTCTT CCGCTCCTC GCTCACTGAC TCGCTGCGCT CGGTGCTTCG 4600  
 GCTGCGGCGA GCGGTATCAG CTCACTCAA GGCGGTAATA CGGTTATCCA 4650  
 50 CAGAATCAGG GGATAACGCA GGAAAGAACA TGTGAGCAA AGGCCAGCAA 4700  
 AAGGCCAGGA ACCGTAAAA GGCCGCGTTG CTGGCGTTTT TCCATAGGCT 4750  
 CCGCCCCCT GACGAGCATC AAAAAATCG ACGCTCAAGT CAGAGGTGGC 4800  
 55 GAAACCCGAC AGGACTATAA AGATACCAGG CGTTTCCCCC TGGAAGCTCC 4850  
 CTCGTGCGCT CTCCTGTTCC GACCCTGCCG CTTACCGGAT ACCTGTCCGC 4900  
 60 CTTTCTCCCT TCGGGAAGCG TGGCGCTTTC TCATAGCTCA CGCTGTAGGT 4950  
 ATCTCAGTTC GGTGTAGGTC GTTCGCTCCA AGCTGGGCTG TGTGCACGAA 5000



CCCCCGTTT AGCCCGACCG CTGCGCCTTA TCCGGTAACT ATCGTCTTGA 5050  
 GTCCAACCCG GTAAGACACG ACTTATCGCC ACTGGCAGCA GCCACTGGTA 5100  
 5 ACAGGATTAG CAGAGCGAGG TATGTAGGCG GTGCTACAGA GTTCTTGAAG 5150  
 TGGTGGCCTA ACTACGGCTA CACTAGAAGG ACAGTATTTG GTATCTGCGC 5200  
 10 TCTGCTGAAG CCAGTTACCT TCGGAAAAAG AGTTGGTAGC TCTTGATCCG 5250  
 GCAAACAAAC CACCGCTGGT AGCGGTGGTT TTTTGTGTTG CAAGCAGCAG 5300  
 ATTACGCGCA GAAAAAAGG ATCTCAAGAA GATCCTTTGA TCTTTTCTAC 5350  
 15 GGGGTCTGAC GCTCAGTGGA ACGAAAACTC ACGTTAAGGG ATTTTGGTCA 5400  
 TGAGATTATC AAAAAGGATC TTCACCTAGA TCCTTTTAAA TTAAAAATGA 5450  
 20 AGTTTTTAAAT CAATCTAAAG TATATATGAG TAAACTTGGT CTGACAGTTA 5500  
 CCAATGCTTA ATCAGTGAGG CACCTATCTC AGCGATCTGT CTATTTCGTT 5550  
 CATCCATAGT TGCCTGACTC CCCGTCGTGT AGATAACTAC GATACGGGAG 5600  
 25 GGCTTACCAT CTGGCCCCAG TGCTGCAATG ATACCGCGAG ACCCACGCTC 5650  
 ACCGGCTCCA GATTTATCAG CAATAAACCA GCCAGCCGGA AGGGCCGAGC 5700  
 30 GCAGAAAGTG TCCTGCAACT TTATCCGCCT CCATCCAGTC TATTAATTGT 5750  
 TGCCGGGAAG CTAGAGTAAG TAGTTCGCCA GTTAATAGTT TGCGCAACGT 5800  
 TGTTGCCATT GCTGCAGGCA TCGTGGTGTC ACGCTCGTCG TTTGGTATGG 5850  
 35 CTTCAATCAG CTCCGGTTCC CAACGATCAA GGCGAGTTAC ATGATCCCCC 5900  
 ATGTTGTGCA AAAAAGCGGT TAGCTCCTTC GGTCTCCGA TCGTTGTCAG 5950  
 40 AAGTAAGTTG GCCGCAGTGT TATCACTCAT GGTTATGGCA GCACTGCATA 6000  
 ATTCTCTTAC TGTCATGCCA TCCGTAAGAT GCTTTTCTGT GACTGGTGAG 6050  
 TACTCAACCA AGTCATTCTG AGAATAGTGT ATGCGGCGAC CGAGTTGCTC 6100  
 45 TTGCCCCGCG TCAACACGGG ATAATACCGC GCCACATAGC AGAACTTTAA 6150  
 AAGTGCTCAT CATTGGAAAA CGTTCTTCGG GGCGAAAACT CTCAAGGATC 6200  
 50 TTACCGCTGT TGAGATCCAG TTCGATGTAA CCCACTCGTG CACCCAACTG 6250  
 ATCTTCAGCA TCTTTTACTT TCACCAGCGT TTCTGGGTGA GCAAAAACAG 6300  
 GAAGGCAAAA TGCCGCAAAA AAGGGAATAA GGGCGACACG GAAATGTTGA 6350  
 55 ATACTCATAC TCTTCCTTTT TCAATATTAT TGAAGCATTT ATCAGGGTTA 6400  
 TTGTCTCATG AGCGGATACA TATTTGAATG TATTTAGAAA AATAAACAAA 6450  
 60 TAGGGGTTC GCGCACATTT CCCCAGAAAAG TGCCACCTGA CGTCTAAGAA 6500  
 ACCATTATTA TCATGACATT AACCTATAAA AATAGGCGTA TCACGAGGCC 6550

CTTTCGTCTT CAA 6563

## (2) INFORMATION FOR SEQ ID NO:62:

## (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 242 amino acids

(B) TYPE: Amino Acid

(D) TOPOLOGY: Linear

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

Met	Lys	Lys	Asn	Ile	Ala	Phe	Leu	Leu	Ala	Ser	Met	Phe	Val	Phe	1	5	10	15
Ser	Ile	Ala	Thr	Asn	Ala	Tyr	Ala	Asp	Ile	Gln	Met	Thr	Gln	Ser	20	25	30	
Pro	Ser	Ser	Leu	Ser	Ala	Ser	Val	Gly	Asp	Arg	Val	Thr	Ile	Thr	35	40	45	
Cys	Arg	Ser	Ser	Gln	Ser	Leu	Val	His	Gly	Ile	Gly	Glu	Thr	Tyr	50	55	60	
Leu	His	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Lys	Ala	Pro	Lys	Leu	Leu	65	70	75	
Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser	Gly	Val	Pro	Ser	Arg	Phe	80	85	90	
Ser	Gly	Ser	Gly	Ser	Gly	Thr	Asp	Phe	Thr	Leu	Thr	Ile	Ser	Ser	95	100	105	
Leu	Gln	Pro	Glu	Asp	Phe	Ala	Thr	Tyr	Tyr	Cys	Ser	Gln	Ser	Thr	110	115	120	
His	Val	Pro	Leu	Thr	Phe	Gly	Gln	Gly	Thr	Lys	Val	Glu	Ile	Lys	125	130	135	
Arg	Thr	Val	Ala	Ala	Pro	Ser	Val	Phe	Ile	Phe	Pro	Pro	Ser	Asp	140	145	150	
Glu	Gln	Leu	Lys	Ser	Gly	Thr	Ala	Ser	Val	Val	Cys	Leu	Leu	Asn	155	160	165	
Asn	Phe	Tyr	Pro	Arg	Glu	Ala	Lys	Val	Gln	Trp	Lys	Val	Asp	Asn	170	175	180	
Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln	Glu	Ser	Val	Thr	Glu	Gln	Asp	185	190	195	
Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Leu	Ser	200	205	210	
Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys	Val	Tyr	Ala	Cys	Glu	Val	Thr	215	220	225	
His	Gln	Gly	Leu	Ser	Ser	Pro	Val	Thr	Lys	Ser	Phe	Asn	Arg	Gly	230	235	240	
Glu	Cys														242			

(2) INFORMATION FOR SEQ ID NO:63:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

CATGGTATAG GTTAACTTA TTTACAC 27

(2) INFORMATION FOR SEQ ID NO:64:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 27 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

CATGGTATAG GTNNSACTTA TTTACAC 27

(2) INFORMATION FOR SEQ ID NO:65:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 780 base pairs  
 (B) TYPE: Nucleic Acid  
 (C) STRANDEDNESS: Single  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ATGAAAAAGA ATATCGCATT TCTTCTTGCA TCTATGTTTCG TTTTTTCTAT 50  
 TGCTACAAAC GCATACGCTG ATATCCAGAT GACCCAGTCC CCGAGCTCCC 100  
 TGTCCGCTC TGTGGGCGAT AGGGTCACCA TCACCTGCAG GTCAAGTCAA 150  
 AGCTTAGTAC ATGGTATAGG TGAGACGTAT TTACACTGGT ATCAACAGAA 200  
 ACCAGGAAAA GCTCCGAAAC TACTGATTTA CAAAGTATCC AATCGATTCT 250  
 CTGGAGTCCC TTCTCGCTTC TCTGGATCCG GTTCTGGGAC GGATTTCACT 300  
 CTGACCATCA GCAGTCTGCA GCCAGAAGAC TTCGCAACTT ATTACTGTTC 350  
 ACAGAGTACT CATGTCCCGC TCACGTTTGG ACAGGGTACC AAGGTGGAGA 400  
 TCAAACGAAC TGTGGCTGCA CCATCTGTCT TCATCTTCCC GCCATCTGAT 450  
 GAGCAGTTGA AATCTGGAAC TGCTTCTGTT GTGTGCCTGC TGAATAACTT 500  
 CTATCCCAGA GAGGCCAAAG TACAGTGGAA GGTGGATAAC GCCCTCCAAT 550  
 CGGGTAACTC CCAGGAGAGT GTCACAGAGC AGGACAGCAA GGACAGCACC 600

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TACAGCCTCA GCAGCACCTT GACGCTGAGC AAAGCAGACT ACGAGAAACA 650  
CAAAGTCTAC GCCTGCGAAG TCACCCATCA GGGCCTGAGC TCGCCCGTCA 700  
5 CAAAGAGCTT CAACAGGGGA GAGTGTTAAG CTGATCCTCT ACGCCGGACG 750  
CATCGTGGCC CTAGTACGCA ACTAGTCGTA 780

(2) INFORMATION FOR SEQ ID NO:66:

10

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

15

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

20

CTAGTGCAGT CTGGCGGTGG CCTGGTGCAG CCAGGGGGCT CACTCCGTTT 50

GTCCTGTGCA GCTTCTGGCT ACTCCTTC 78

(2) INFORMATION FOR SEQ ID NO:67:

25

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

30

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

35

TCGAGAAGGA GTAGCCAGAA GCTGCACAGG ACAAACGGAG TGAGCCCCCT 50

GGCTGCACCA GGCCACCGCC AGACTGCACT AG 82

(2) INFORMATION FOR SEQ ID NO:68:

40

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 8120 base pairs

(B) TYPE: Nucleic Acid

(C) STRANDEDNESS: Single

45

(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

50

TTCGAGCTCG CCCGACATTG ATTATTGACT AGAGTCGATC GACAGCTGTG 50

GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 100

GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAG 150

55

TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 200

GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 250

60

CGCCCAGTTC CGCCCATTCT CCGCCCCATG GCTGACTAAT TTTTTTTATT 300

TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 350

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      AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAAGCTA GCTTATCCGG 400
      CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTGACGTAA 450
5     GTACCGCCTA TAGAGCGATA AGAGGATTTT ATCCCCGCTG CCATCATGGT 500
      TCGACCATTG AACTGCATCG TCGCCGTGTC CCAAAATATG GGGATTGGCA 550
10    AGAACGGAGA CCTACCCTGG CCTCCGCTCA GGAACGAGTT CAAGTACTTC 600
      CAAAGAATGA CCACAACCTC TTCAGTGGAA GGTAAACAGA ATCTGGTGAT 650
      TATGGGTAGG AAAACCTGGT TCTCCATTCC TGAGAAGAAT CGACCTTTAA 700
15    AGGACAGAAT TAATATAGTT CTCAGTAGAG AACTCAAAGA ACCACCACGA 750
      GGAGCTCATT TTCTTGCCAA AAGTTTGGAT GATGCCTTAA GACTTATTGA 800
20    ACAACCGGAA TTGGCAAGTA AAGTAGACAT GGTTTGGATA GTCGGAGGCA 850
      GTTCTGTTTA CCAGGAAGCC ATGAATCAAC CAGGCCACCT TAGACTCTTT 900
      GTGACAAGGA TCATGCAGGA ATTTGAAAGT GACACGTTTT TCCAGAAAT 950
25    TGATTTGGGG AAATATAAAC CTCTCCCAGA ATACCCAGGC GTCCTCTCTG 1000
      AGGTCCAGGA GGAAAAAGGC ATCAAGTATA AGTTTGAAGT CTACGAGAAG 1050
30    AAAGACTAAC AGGAAGATGC TTTCAAGTTC TCTGCTCCCC TCCTAAAGCT 1100
      ATGCATTTTT ATAAGACCAT GGGACTTTTG CTGGCTTTAG ATCCCCTTGG 1150
      CTTCGTTAGA ACGCAGCTAC AATTAATACA TAACCTTATG TATCATAAC 1200
35    ATACGATTTA GGTGACACTA TAGATAACAT CCACTTTGCC TTTCTCTCCA 1250
      CAGGTGTCCA CTCCCAGGTC CAACTGCACC TCGGTTCTAT CGATTGAATT 1300
40    CCACCATGGG ATGGTCATGT ATCATCCTTT TTCTAGTAGC AACTGCAACT 1350
      GGAGTACATT CAGAAGTTCA GCTAGTGCAG TCTGGCGGTG GCCTGGTGCA 1400
      GCCAGGGGGC TCACTCCGTT TGTCCTGTGC AGCTTCTGGC TACTCCTTCT 1450
45    CGAGTCACTA TATGCACTGG GTCCGTCAGG CCCCGGGTAA GGCCTGGAA 1500
      TGGGTTGGAT ATATTGATCC TTCCAATGGT GAAACTACGT ATAATCAAAA 1550
50    GTTCAAGGGC CGTTTCACTT TATCTCGCGA CAACTCCAAA AACACAGCAT 1600
      ACCTGCAGAT GAACAGCCTG CGTGCTGAGG AACTGCCGT CTATTACTGT 1650
      GCAAGAGGGG ATTATCGCTA CAATGGTGAC TGGTTCTTCG ACGTCTGGGG 1700
55    TCAAGGAACC CTGGTCACCG TCTCCTCGGC CTCCACCAAG GGCCCATCGG 1750
      TCTTCCCCCT GGCACCCTCC TCCAAGAGCA CCTCTGGGGG CACAGCGGCC 1800
60    CTGGGCTGCC TGGTCAAGGA CTACTTCCCC GAACCGGTGA CGGTGTCGTG 1850
      GAACTCAGGC GCCCTGACCA GCGGCGTGCA CACCTTCCCG GCTGTCCTAC 1900

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AGTCCTCAGG ACTCTACTCC CTCAGCAGCG TGGTGACTGT GCCCTCTAGC 1950  
 AGCTTGGGCA CCCAGACCTA CATCTGCAAC GTGAATCACA AGCCCAGCAA 2000  
 5 CACCAAGGTG GACAAGAAAG TTGAGCCCAA ATCTTGTGAC AAAACTCACA 2050  
 CATGCCCACC GTGCCCAGCA CCTGAACTCC TGGGGGGACC GTCAGTCTTC 2100  
 10 CTCTTCCCCC CAAAACCCAA GGACACCCTC ATGATCTCCC GGACCCCTGA 2150  
 GGTACATGCG GTGGTGGTGG ACGTGAGCCA CGAAGACCCT GAGGTCAAGT 2200  
 TCAACTGGTA CGTGGACGGC GTGGAGGTGC ATAATGCCAA GACAAAGCCG 2250  
 15 CGGGAGGAGC AGTACAACAG CACGTACCGT GTGGTCAGCG TCCTCACCCT 2300  
 CCTGCACCAG GACTGGCTGA ATGGCAAGGA GTACAAGTGC AAGGTCTCCA 2350  
 20 ACAAAGCCCT CCCAGCCCCC ATCGAGAAAA CCATCTCCAA AGCCAAAGGG 2400  
 CAGCCCCGAG AACCACAGGT GTACACCCTG CCCCATCCC GGGAAAGAGAT 2450  
 GACCAAGAAC CAGGTCAGCC TGACCTGCCT GGTCAAAGGC TTCTATCCCA 2500  
 25 GCGACATCGC CGTGGAGTGG GAGAGCAATG GGCAGCCGGA GAACAACTAC 2550  
 AAGACCACGC CTCCCGTGCT GGACTCCGAC GGCTCCTTCT TCCTCTACAG 2600  
 30 CAAGCTCACC GTGGACAAGA GCAGGTGGCA GCAGGGGAAC GTCTTCTCAT 2650  
 GCTCCGTGAT GCATGAGGCT CTGCACAACC ACTACACGCA GAAGAGCCTC 2700  
 TCCCTGTCTC CGGGTAAATG AGTGCGACGG CCCTAGAGTC GACCTGCAGA 2750  
 35 AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT AATGGTTACA 2800  
 AATAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT TTTTCTACTG 2850  
 40 CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT ATCATGTCTG 2900  
 GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA AATAACCTCT 2950  
 GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA ACCATCTGTG 3000  
 45 GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC CCAGCAGGCA 3050  
 GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG GTGTGGAAAAG 3100  
 50 TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC ATCTCAATTA 3150  
 GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG CCCCTAACTC 3200  
 CGCCAGTTC CGCCCATCTT CCGCCCCATG GCTGACTAAT TTTTTTTATT 3250  
 55 TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC AGAAGTAGTG 3300  
 AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGCTA GCTTATCCGG 3350  
 60 CCGGGAACGG TGCATTGGAA CGCGGATTCC CCGTGCCAAG AGTCAGGTAA 3400  
 GTACCGCCTA TAGAGTCTAT AGGCCACCC CTTGGCTTC GTTAGAACGC 3450

GGCTACAATT AATACATAAC CTTTTGGATC GATCCTACTG AACTGACAT 3500  
 5 CCACTTTTTTC TTTTCTCCA CAGGTGTCCA CTCCCAGGTC CAACTGCACC 3550  
 TCGGTTTCGCG AAGCTAGCTT GGGCTGCATC GATTGAATTC CACCATGGGA 3600  
 TGGTCATGTA TCATCCTTTT TCTAGTAGCA ACTGCAACTG GAGTACATTC 3650  
 10 AGATATCCAG ATGACCCAGT CCCCAGGCTC CCTGTCCGCC TCTGTGGGCG 3700  
 ATAGGGTCAC CATCACCTGC AGGTCAAGTC AAAGCTTAGT ACATGGTATA 3750  
 GGTGCTACGT ATTTACTACTG GTATCAACAG AAACCAGGAA AAGCTCCGAA 3800  
 15 ACTACTGATT TACAAAGTAT CCAATCGATT CTCTGGAGTC CCTTCTCGCT 3850  
 TCTCTGGATC CGGTTCTGGG ACGGATTTCA CTCTGACCAT CAGCAGTCTG 3900  
 20 CAGCCAGAAG ACTTCGCAAC TTATTACTGT TCACAGAGTA CTCATGTCCC 3950  
 GCTCACGTTT GGACAGGGTA CCAAGGTGGA GATCAAACGA ACTGTGGCTG 4000  
 CACCATCTGT CTTTCATCTTC CCGCCATCTG ATGAGCAGTT GAAATCTGGA 4050  
 25 ACTGCTTCTG TTGTGTGCCT GCTGAATAAC TTCTATCCCA GAGAGGCCAA 4100  
 AGTACAGTGG AAGGTGGATA ACGCCCTCCA ATCGGGTAAC TCCCAGGAGA 4150  
 30 GTGTCACAGA GCAGGACAGC AAGGACAGCA CCTACAGCCT CAGCAGCACC 4200  
 CTGACGCTGA GCAAAGCAGA CTACGAGAAA CACAAAGTCT ACGCCTGCGA 4250  
 AGTCACCCAT CAGGGCCTGA GCTCGCCCGT CACAAAGAGC TTCAACAGGG 4300  
 35 GAGAGTGTTA AGCTTGGCCG CCATGGCCCA ACTTGTTTAT TGCAGCTTAT 4350  
 AATGGTTACA AATAAAGCAA TAGCATCACA AATTTACAA ATAAAGCATT 4400  
 40 TTTTTCCTG CATTCTAGTT GTGGTTTGTC CAAACTCATC AATGTATCTT 4450  
 ATCATGTCTG GATCGATCGG GAATTAATTC GGCGCAGCAC CATGGCCTGA 4500  
 AATAACCTCT GAAAGAGGAA CTTGGTTAGG TACCTTCTGA GGCGGAAAGA 4550  
 45 ACCAGCTGTG GAATGTGTGT CAGTTAGGGT GTGGAAAGTC CCCAGGCTCC 4600  
 CCAGCAGGCA GAAGTATGCA AAGCATGCAT CTCAATTAGT CAGCAACCAG 4650  
 50 GTGTGGAAAG TCCCCAGGCT CCCCAGCAGG CAGAAGTATG CAAAGCATGC 4700  
 ATCTCAATTA GTCAGCAACC ATAGTCCCGC CCCTAACTCC GCCCATCCCG 4750  
 CCCCTAACTC CGCCCAGTTC CGCCCATCTT CCGCCCCATG GCTGACTAAT 4800  
 55 TTTTTTTTATT TATGCAGAGG CCGAGGCCGC CTCGGCCTCT GAGCTATTCC 4850  
 AGAAGTAGTG AGGAGGCTTT TTTGGAGGCC TAGGCTTTTG CAAAAGCTG 4900  
 60 TTACCTCGAG CGGCCGCTTA ATTAAGGCGC GCCATTTAAA TCCTGCAGGT 4950  
 AACAGCTTGG CACTGGCCGT CGTTTTACAA CGTCGTGACT GGGAAAACCC 5000

TGGCGTTACC CAACTTAATC GCCTTGCAGC ACATCCCCC TTCGCCAGCT 5050  
 5 GGC GTAATAG CGAAGAGGCC CGCACCGATC GCCCTTCCCA ACAGTTGCGT 5100  
 AGCCTGAATG GCGAATGGCG CCTGATGCGG TATTTTCTCC TTACGCATCT 5150  
 GTGCGGTATT TCACACCGCA TACGTCAAAG CAACCATAGT ACGCGCCCTG 5200  
 10 TAGCGGCGCA TTAAGCGCGG CGGGTGTGGT GGTACGCGC AGCGTGACCG 5250  
 CTACACTTGC CAGCGCCCTA GCGCCCGCTC CTTTCGCTTT CTTCCCTTCC 5300  
 TTTCTCGCCA CGTTCGCCCG CTTTCCCCGT CAAGCTCTAA ATCGGGGGCT 5350  
 15 CCCTTTAGGG TTCCGATTTA GTGCTTTACG GCACCTCGAC CCCAAAAAAC 5400  
 TTGATTTGGG TGATGGTTCA CGTAGTGGGC CATCGCCCTG ATAGACGGTT 5450  
 20 TTTCGCCCTT TGACGTTGGA GTCCACGTTT TTTAATAGTG GACTCTTGTT 5500  
 CCAAACCTGA ACAACACTCA ACCCTATCTC GGGCTATTCT TTTGATTTAT 5550  
 AAGGGATTTT GCCGATTTTC GCCTATTGGT TAAAAAATGA GCTGATTTAA 5600  
 25 CAAAAATTTA ACGCGAATTT TAACAAAATA TTAACGTTTA CAATTTTATG 5650  
 GTGCACTCTC AGTACAATCT GCTCTGATGC CGCATAGTTA AGCCAACTCC 5700  
 30 GCTATCGCTA CGTGA CTGGG TCATGGCTGC GCCCCGACAC CCGCCAACAC 5750  
 CCGCTGACGC GCCCTGACGG GCTTGTCTGC TCCCGGCATC CGCTTACAGA 5800  
 CAAGCTGTGA CCGTCTCCGG GAGCTGCATG TGTCAGAGGT TTTCAACGTC 5850  
 35 ATCACCGAAA CGCGCGAGGC AGTATTCTTG AAGACGAAAG GGCCTCGTGA 5900  
 TACGCCTATT TTTATAGGTT AATGTCATGA TAATAATGGT TTCTTAGACG 5950  
 40 TCAGGTGGCA CTTTTCGGGG AAATGTGCGC GGAACCCCTA TTTGTTTATT 6000  
 TTTCTAAATA CATTCAAATA TGTATCCGCT CATGAGACAA TAACCCTGAT 6050  
 AAATGCTTCA ATAATATTGA AAAAGGAAGA GTATGAGTAT TCAACATTTT 6100  
 45 CGTGTCGCCC TTATTCCCTT TTTTGC GGCA TTTTGCCTTC CTGTTTTTGC 6150  
 TCACCCAGAA ACGCTGGTGA AAGTAAAAGA TGCTGAAGAT CAGTTGGGTG 6200  
 50 CACGAGTGGG TTACATCGAA CTGGATCTCA ACAGCGGTAA GATCCTTGAG 6250  
 AGTTTTTCGCC CCGAAGAACG TTTTCCAATG ATGAGCACTT TTAAAGTTCT 6300  
 GCTATGTGGC GCGGTATTAT CCCGTGATGA CGCCGGGCAA GAGCAACTCG 6350  
 55 GTCGCCGCAT ACACTATTCT CAGAATGACT TGGTTGAGTA CTCACCAGTC 6400  
 ACAGAAAAGC ATCTTACGGA TGGCATGACA GTAAGAGAAT TATGCAGTGC 6450  
 60 TGCCATAACC ATGAGTGATA AACTGCGGC CAACTTACTT CTGACAACGA 6500  
 TCGGAGGACC GAAGGAGCTA ACCGCTTTTT TGCACAACAT GGGGGATCAT 6550



5      GTAACTCGCC TTGATCGTTG GGAACCGGAG CTGAATGAAG CCATACCAAA 6600  
 CGACGAGCGT GACACCACGA TGCCAGCAGC AATGGCAACA ACGTTGCGCA 6650  
 AACTATTAAC TGGCGAACTA CTTACTCTAG CTTCCCGGCA ACAATTAATA 6700  
 GACTGGATGG AGGCGGATAA AGTTGCAGGA CCACTTCTGC GCTCGGCCCT 6750  
 10    TCCGGCTGGC TGGTTTATTTG CTGATAAATC TGGAGCCGGT GAGCGTGGGT 6800  
 CTCGCGGTAT CATTCAGCA CTGGGGCCAG ATGGTAAGCC CTCCCGTATC 6850  
 GTAGTTATCT ACACGACGGG GAGTCAGGCA ACTATGGATG AACGAAATAG 6900  
 15    ACAGATCGCT GAGATAGGTG CCTCACTGAT TAAGCATTGG TAACTGTCAG 6950  
 ACCAAGTTTA CTCATATATA CTTTAGATTG ATTTAAAACT TCATTTTTTAA 7000  
 20    TTTAAAAGGA TCTAGGTGAA GATCCTTTTT GATAATCTCA TGACCAAAAT 7050  
 CCCTTAACGT GAGTTTTTCGT TCCACTGAGC GTCAGACCCC GTAGAAAAGA 7100  
 TCAAAGGATC TTCTTGAGAT CCTTTTTTTC TGCGCGTAAT CTGCTGCTTG 7150  
 25    CAAACAAAAA AACCACCGCT ACCAGCGGTG GTTTGTTTGC CGGATCAAGA 7200  
 GCTACCAACT CTTTTTCCGA AGGTAAGTGG CTTTCAAGCA GCGCAGATAC 7250  
 30    CAAATACTGT CCTTCTAGTG TAGCCGTAGT TAGGCCACCA CTTCAAGAAC 7300  
 TCTGTAGCAC CGCCTACATA CCTCGCTCTG CTAATCCTGT TACCAGTGGC 7350  
 TGCTGCCAGT GGCATAAGT CGTGTCTTAC CGGGTTGGAC TCAAGACGAT 7400  
 35    AGTTACCGGA TAAGGCGCAG CGGTCGGGCT GAACGGGGGG TTCGTGCACA 7450  
 CAGCCCAGCT TGGAGCGAAC GACCTACACC GAACTGAGAT ACCTACAGCG 7500  
 40    TGAGCATTGA GAAAGCGCCA CGCTTCCCGA AGGGAGAAAG GCGGACAGGT 7550  
 ATCCGGTAAG CGGCAGGGTC GGAACAGGAG AGCGCACGAG GGAGCTTCCA 7600  
 GGGGGAAACG CCTGGTATCT TTATAGTCCT GTCGGGTTTC GCCACCTCTG 7650  
 45    ACTTGAGCGT CGATTTTTGT GATGCTCGTC AGGGGGGCGG AGCCTATGGA 7700  
 AAAACGCCAG CAACGCGGCC TTTTACGGT TCCTGGCCTT TTGCTGGCCT 7750  
 50    TTTGCTCACA TGTCTTTTCC TGCATTATCC CCTGATTCTG TGGATAACCG 7800  
 TATTACCGCC TTTGAGTGAG CTGATACCGC TCGCCGCAGC CGAACGACCG 7850  
 AGCGCAGCGA GTCAGTGAGC GAGGAAGCGG AAGAGCGCCC AATACGCAAA 7900  
 55    CCGCCTCTCC CCGCGCGTTG GCCGATTAT TAATCCAGCT GGCACGACAG 7950  
 GTTTCCCGAC TGGAAAGCGG GCAGTGAGCG CAACGCAATT AATGTGAGTT 8000  
 60    ACCTCACTCA TTAGGCACCC CAGGCTTTAC ACTTTATGCT TCCGGCTCGT 8050  
 ATGTTGTGTG GAATTGTGAG CGGATAACAA TTTCACACAG GAAACAGCTA 8100

TGACCATGAT TACGAATTAA 8120

(2) INFORMATION FOR SEQ ID NO:69:

5

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 800 base pairs
  - (B) TYPE: Nucleic Acid
  - (C) STRANDEDNESS: Single
  - (D) TOPOLOGY: Linear

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

15 AAAAGGGTAT CTAGAGGTTG AGGTGATTTT ATGAAAAAGA ATATCGCATT 50  
 TCTTCTTGCA TCTATGTTCTG TTTTCTCTAT TGCTACAAAC GCGTACGCTG 100  
 AGGTTTCAGCT AGTGCAGTCT GGCAGGTGGCC TGGTGCAGCC AGGGGGCTCA 150  
 20 CTCCGTTTGT CCTGTGCAGC TTCTGGCTAC TCCTTCTCGA GTCACATATAT 200  
 GCACTGGGTC CGTCAGGCCC CGGGTAAGGG CCTGGAATGG GTTGGATATA 250  
 25 TTGATCCTTC CAATGGTGAA ACTACGTATA ATCAAAAGTT CAAGGGCCGT 300  
 TTCACTTTAT CTCGCGACAA CTCCAAAAAC ACAGCATACC TGCAGATGAA 350  
 CAGCCTGCGT GCTGAGGACA CTGCCGTCTA TTACTGTGCA AGAGGGGATT 400  
 30 ATCGCTACAA TGGTGACTGG TTCTTCGACG TCTGGGGTCA AGGAACCCTG 450  
 GTCACCGTCT CCTCGGCCTC CACCAAGGGC CCATCGGTCT TCCCCCTGGC 500  
 35 ACCCTCCTCC AAGAGCACCT CTGGGGGCAC AGCGGCCCTG GGCTGCCTGG 550  
 TCAAGGACTA CTTCCCCGAA CCGGTGACGG TGTCGTGGAA CTCAGGCGCC 600  
 CTGACCAGCG GCGTGACAC CTTCCCGGCT GTCCTACAGT CCTCAGGACT 650  
 40 CTACTCCCTC AGCAGCGTGG TGACCGTGCC CTCCAGCAGC TTGGGCACCC 700  
 AGACCTACAT CTGCAACGTG AATCACAAGC CCAGCAACAC CAAGGTCGAC 750  
 45 AAGAAAGTTG AGCCCAAATC TTGTGACAAA ACTCACACAT GCCCGCCTGA 800

(2) INFORMATION FOR SEQ ID NO:70:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 256 amino acids
  - (B) TYPE: Amino Acid
  - (D) TOPOLOGY: Linear

50

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

55

Met Lys Lys Asn Ile Ala Phe Leu Leu Ala Ser Met Phe Val Phe  
 1 5 10 15  
 Ser Ile Ala Thr Asn Ala Tyr Ala Glu Val Gln Leu Val Gln Ser  
 60 20 25 30  
 Gly Gly Gly Leu Val Gln Pro Gly Gly Ser Leu Arg Leu Ser Cys

	35	40	45
	Ala Ala Ser Gly Tyr Ser Phe Ser Ser His Tyr Met His Trp Val		
	50	55	60
5	Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Gly Tyr Ile Asp		
	65	70	75
	Pro Ser Asn Gly Glu Thr Thr Tyr Asn Gln Lys Phe Lys Gly Arg		
10	80	85	90
	Phe Thr Leu Ser Arg Asp Asn Ser Lys Asn Thr Ala Tyr Leu Gln		
	95	100	105
15	Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys Ala		
	110	115	120
	Arg Gly Asp Tyr Arg Tyr Asn Gly Asp Trp Phe Phe Asp Val Trp		
20	125	130	135
	Gly Gln Gly Thr Leu Val Thr Val Ser Ser Ala Ser Thr Lys Gly		
	140	145	150
	Pro Ser Val Phe Pro Leu Ala Pro Ser Ser Lys Ser Thr Ser Gly		
25	155	160	165
	Gly Thr Ala Ala Leu Gly Cys Leu Val Lys Asp Tyr Phe Pro Glu		
	170	175	180
30	Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu Thr Ser Gly Val		
	185	190	195
	His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu Tyr Ser Leu		
35	200	205	210
	Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr Gln Thr		
	215	220	225
	Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val Asp		
40	230	235	240
	Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro		
	245	250	255
45	Pro		
	256		

## (2) INFORMATION FOR SEQ ID NO:71:

50 (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 452 amino acids  
 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

	Glu Val Gln Leu Val Gln Ser Gly Gly Gly Leu Val Gln Pro Gly		
	1	5	10
60	Gly Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Tyr Ser Phe Ser		
	20	25	30

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	Ser	His	Tyr	Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	
					35					40						45
5	Glu	Trp	Val	Gly	Tyr	Ile	Asp	Pro	Ser	Asn	Gly	Glu	Thr	Thr	Tyr	
					50					55						60
	Asn	Gln	Lys	Phe	Lys	Gly	Arg	Phe	Thr	Leu	Ser	Arg	Asp	Asn	Ser	
					65					70						75
10	Lys	Asn	Thr	Ala	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	Ala	Glu	Asp	
					80					85						90
	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Gly	Asp	Tyr	Arg	Tyr	Asn	Gly	
15					95					100						105
	Asp	Trp	Phe	Phe	Asp	Val	Trp	Gly	Gln	Gly	Thr	Leu	Val	Thr	Val	
					110					115						120
20	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	Ala	Pro	
					125					130						135
	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	Leu	
					140					145						150
25	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
					155					160						165
	Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	
30					170					175						180
	Ser	Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	
					185					190						195
35	Ser	Ser	Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	
					200					205						210
	Pro	Ser	Asn	Thr	Lys	Val	Asp	Lys	Lys	Val	Glu	Pro	Lys	Ser	Cys	
					215					220						225
40	Asp	Lys	Thr	His	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro	Glu	Leu	Leu	
					230					235						240
	Gly	Gly	Pro	Ser	Val	Phe	Leu	Phe	Pro	Pro	Lys	Pro	Lys	Asp	Thr	
45					245					250						255
	Leu	Met	Ile	Ser	Arg	Thr	Pro	Glu	Val	Thr	Cys	Val	Val	Val	Asp	
					260					265						270
50	Val	Ser	His	Glu	Asp	Pro	Glu	Val	Lys	Phe	Asn	Trp	Tyr	Val	Asp	
					275					280						285
	Gly	Val	Glu	Val	His	Asn	Ala	Lys	Thr	Lys	Pro	Arg	Glu	Glu	Gln	
					290					295						300
55	Tyr	Asn	Ser	Thr	Tyr	Arg	Val	Val	Ser	Val	Leu	Thr	Val	Leu	His	
					305					310						315
	Gln	Asp	Trp	Leu	Asn	Gly	Lys	Glu	Tyr	Lys	Cys	Lys	Val	Ser	Asn	
60					320					325						330
	Lys	Ala	Leu	Pro	Ala	Pro	Ile	Glu	Lys	Thr	Ile	Ser	Lys	Ala	Lys	
					335					340						345

Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg  
 350 355 360  
 5 Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys  
 365 370 375  
 Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly  
 380 385 390  
 10 Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser  
 395 400 405  
 Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser  
 15 410 415 420  
 Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu  
 425 430 435  
 20 Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro  
 440 445 450

Gly Lys  
 452

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(2) INFORMATION FOR SEQ ID NO:72:

(i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 219 amino acids  
 30 (B) TYPE: Amino Acid  
 (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

35 Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala Ser Val  
 1 5 10 15  
 Gly Asp Arg Val Thr Ile Thr Cys Arg Ser Ser Gln Ser Leu Val  
 20 25 30  
 40 His Gly Ile Gly Ala Thr Tyr Leu His Trp Tyr Gln Gln Lys Pro  
 35 40 45  
 45 Gly Lys Ala Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe  
 50 55 60  
 Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp  
 65 70 75  
 50 Phe Thr Leu Thr Ile Ser Ser Leu Gln Pro Glu Asp Phe Ala Thr  
 80 85 90  
 Tyr Tyr Cys Ser Gln Ser Thr His Val Pro Leu Thr Phe Gly Gln  
 95 100 105  
 55 Gly Thr Lys Val Glu Ile Lys Arg Thr Val Ala Ala Pro Ser Val  
 110 115 120  
 Phe Ile Phe Pro Pro Ser Asp Glu Gln Leu Lys Ser Gly Thr Ala  
 60 125 130 135  
 Ser Val Val Cys Leu Leu Asn Asn Phe Tyr Pro Arg Glu Ala Lys

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				140					145					150	
	Val	Gln	Trp	Lys	Val	Asp	Asn	Ala	Leu	Gln	Ser	Gly	Asn	Ser	Gln
				155						160					165
5	Glu	Ser	Val	Thr	Glu	Gln	Asp	Ser	Lys	Asp	Ser	Thr	Tyr	Ser	Leu
				170						175					180
	Ser	Ser	Thr	Leu	Thr	Leu	Ser	Lys	Ala	Asp	Tyr	Glu	Lys	His	Lys
10				185						190					195
	Val	Tyr	Ala	Cys	Glu	Val	Thr	His	Gln	Gly	Leu	Ser	Ser	Pro	Val
				200						205					210
15	Thr	Lys	Ser	Phe	Asn	Arg	Gly	Glu	Cys						
				215					219						